ALBERT FRADERA SOLA

I consider myself both collaborative and adaptable. I am always eager to tackle new and different projects. I am very enthusiastic to always share and develop my data visualization skills as a means towards better scientific communication. I am an open-minded person and enjoy having great relationships with my colleagues.

EDUCATION

Current | 2018

PhD Candidate in Quantitative Proteomics
JGU University — Mainz, Germany

- PhD thesis: Computational approaches to mass spectrometry based quantitative proteomics

2017 | 2016

M.Sc. in Omics Data Analysis
University of Vic — Barcelona, Spain

- Master thesis: Development of a scoring function for finding differential expression - application to Lolium Perenne
- Erasmus + grant fellow

RESEARCH EXPERIENCE

Current | 2018

PhD Candidate
Butter laboratory - Institure Molecular Biology — Mainz, Germany

- PhD candidate with Dr. Falk Butter (F.Butter@imb-mainz.de)
- Publications: 1 first-author paper (in submission), 5 co-author papers

2017

Master Student
Narcis Fernandez-Fuentes - IBERS — Aberystwyth, UK

- MSc student with Dr. Narcs Fernandez-Fuentes (naf4@aber.ac.uk)
- Publications: 1 first-authtor paper, 1 co-author paper

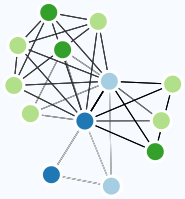
WET LAB PROJECTS AND RELATED SKILLS

Immunoprecipitation of RNA-binding proteins in S. cerevisiae

- I was responsible for designing the experimental setup and generating the data for the RNA-binding protein interactome investigation.
- Keywords: Yeast | Protein Immunoprecipitation | Experimental design

Mass spectrometry quantitative proteomics

- I used chemical labeling (DML) and label-free mass spectrometry sample preparation protocols on several projects
- Keyword: Mass spectrometry | DML | LFQ | In-gel digestion



My CV as an interactive network

Bullet points (Blue, for and , and green, for and) are linked by year. Interactive version here

CONTACT

AFraderaSola

A.FraderaSola@imb.de

+49 179 3469988

SOFTWARE SKILLS

- R
- MaxQuant
- Bash
- Python

LANGUAGE SKILLS

- Catalan
- Spanish
- English
- German

DRY LAB PROJECTS AND RELATED SKILLS

Network-based assignment of RNA-binding proteins functionality

- Function-based networks were created from quantitative proteomics data and made accessible through a shiny app.
- Keywords: Network | Functional analysis | KEGG | GO | R Shiny

Temporal proteome profiling of Xenopus and Leismania species

- Differential expression of proteomes was investigated at various stages
- Clustering (Self Organizing Maps) and dimesionality reduction techniques (Principal Component Analysis) were applied.
- Keywords: Proteome | Differential expression | SOM | PCA | Clustering

Scoring function for RNA-Seq differential expression assessment

- A scoring function was developed around three RNA-Seq differential expression assessment R packages (DESeq2, edgeR, limma+voom)
- Keywords: NGS | RNA-Seq | Quality control | Differential expression

ChIP-Seq characterization of a novel ATPase in T. brucei

- H2A.Z deposition was investigated and visualized with genome tracks
- Keywords: NGS | ChIP-Seq | Genome tracks

SELECTED PUBLICATIONS

Projects with Genomics Analysis

- 2022 | PLoS Pathogens | https://doi.org/10.1371/journal.ppat.1010514
- 2021 | Nature Comunications | https://doi.org/10.1038/s41467-021-22861-2
- 2021 | PLoS One | https://doi.org/10.1371/journal.pone.0249636
- 2019 | PLoS One | https://doi.org/10.1371/journal.pone.0220518

Projects with Proteomics Analysis

- 2021 | Journal of Cell Science | https://doi.org/10.1242/jcs.254300
- 2020 | RNA | https://doi.org/10.1261/rna.076281.120

Publication abstract's wordcloud

CONFERENCES AND COURSES

Conferences

- 2022 | Statistical data analysis for genome-scale biology |Flash talk
- 2021 | Network biology |Plenary talk
- 2019 | FEBS advanced course |Poster presentation

Courses

- 2022 | Data visualization for scientists
- 2021 | Scientific writing
- 2020 | Convincing scientific presentations

Document created with the R packages pagedown and datadrivencv.

The source code is available on github.

Last updated on 2022-07-24.